

WE CLAIM:

1. A method for selecting a therapeutic regimen for treating a cancer in a patient wherein a chemotherapeutic drug is administered to the patient, the method comprising screening a suitable cell or tissue sample isolated from said patient for a genomic polymorphism or genotype that is correlative to treatment outcome of the cancer.
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2. The method of claim 1, wherein the cancer is a cancer that can be treated by the administration of a chemotherapeutic drug selected from the group consisting of fluoropyrimidine or a platinum drug.
- 10 3. The method of claim 1, wherein the cancer is selected from the group consisting of esophageal cancer, gastric cancer, colon cancer, rectal cancer, colorectal cancer and lung cancer.
4. The method of claim 2, wherein the cancer treatment further comprises radiation therapy.
- 15 5. The method of claim 1, wherein said genomic polymorphism occurs in the gene selected from the group consisting of thymidylate synthase gene, excision repair complementation group gene (ERCC1), VEGF, ERC2 gene, XRCC-1 gene, human glutathione s-transferase P1 gene, epidermal growth factor receptor gene, matrix metalloproteinase genes (-1, and -3), interleukin 8 (IL-8) gene, D-pyrimidine dehydrogenase (DPD) and CXC chemokine.
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6. The method of claim 5, wherein the genotype is high expression of a gene selected from the group consisting of thymidylate synthase, D-pyrimidine dehydrogenase (DPD) ERCC1 and VEGF and said tissue sample is normal tissue that corresponds to the tumor type. drug to treat the cancer.
- 25 7. A method for reducing chemically induced neurotoxicity associated with cancer chemotherapy in a patient comprising administering to said subject an effective amount of a COX-2 inhibitor to a patient in need thereof.
8. The method of claim 7, wherein the chemotherapy comprises administration of oxaliplatin.

9. The method of claim 7, wherein the chemotherapy comprises administration of 5-FU.
10. A method for determining if a human patient is more likely to experience tumor recurrence after surgical removal of said tumor, comprising determining the expression level of a gene selected from the group consisting of TS, DPD, ERCC1 and VEGF, in a cell or sample isolated from normal tissue adjacent to said tumor and correlating said expression level with normal levels, wherein overexpression of said gene is predictive to identify patients at risk for tumor recurrence.
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11. The method of claim 11, wherein the tumor is associated with rectal cancer.